APPROVED BY DRAFTSMAN | C.G. FIG. | CLASS | SUBCLASS

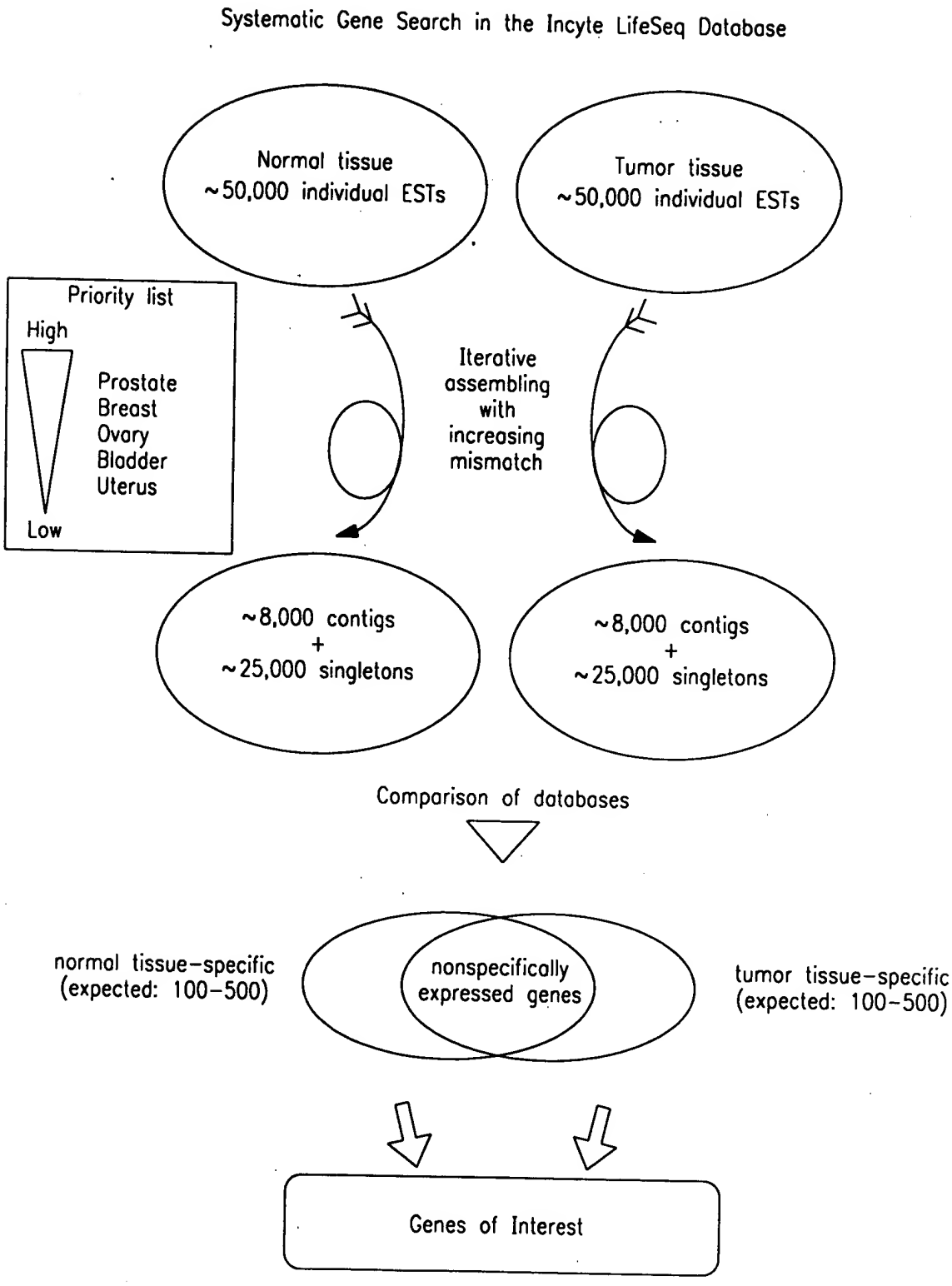


FIG. 1

APPROVED O.G. FIG.
BY | CLASS | SUBCLASS
DRAFTSMAN

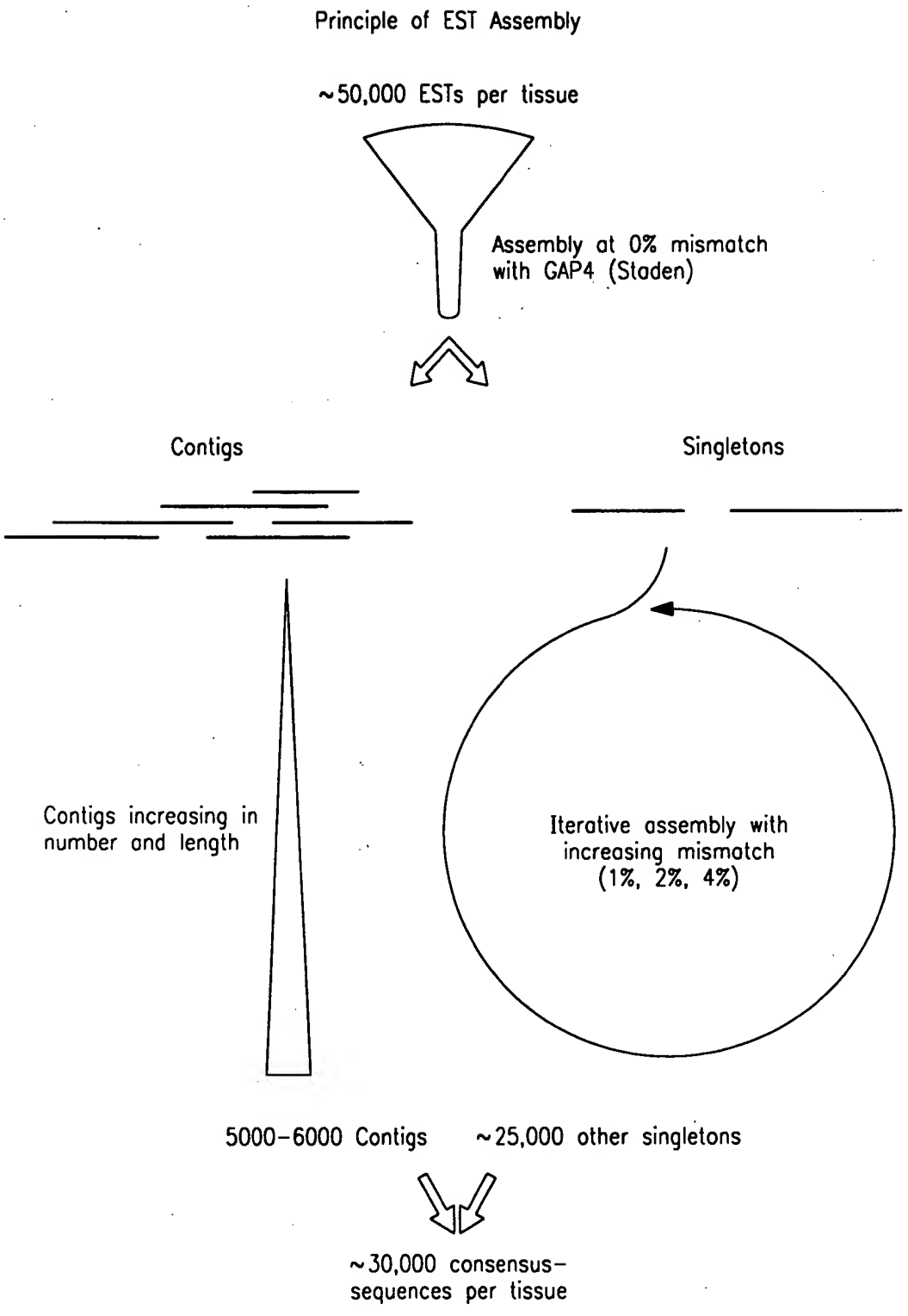


FIG. 2a

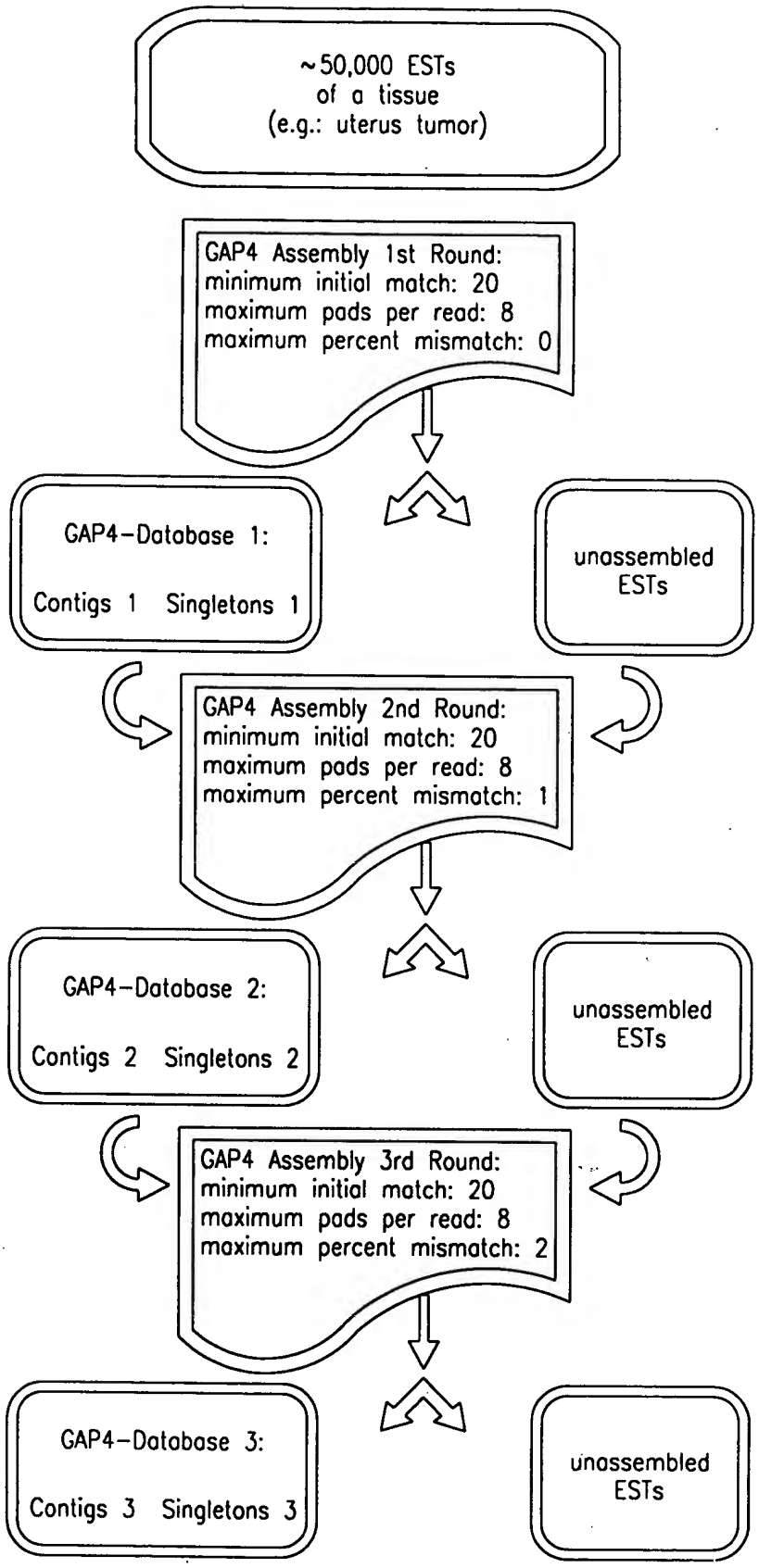

~50,000 ESTs
of a tissue
(e.g.: uterus tumor)
GAP4 Assembly 1st Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 0
GAP4-Database 1:
Contigs 1 Singletons 1
unassembled
ESTs
GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 1
GAP4-Database 2:
Contigs 2 Singletons 2
unassembled
ESTs
GAP4 Assembly 3rd Round:
minimum initial match: 20
maximum pads per read: 8
maximum percent mismatch: 2
GAP4-Database 3:
Contigs 3 Singletons 3
unassembled
ESTs

FIG. 2b-I

APPROVED BY DRAFTSMAN
O.G. FIG.
CLASS SUBCLASS

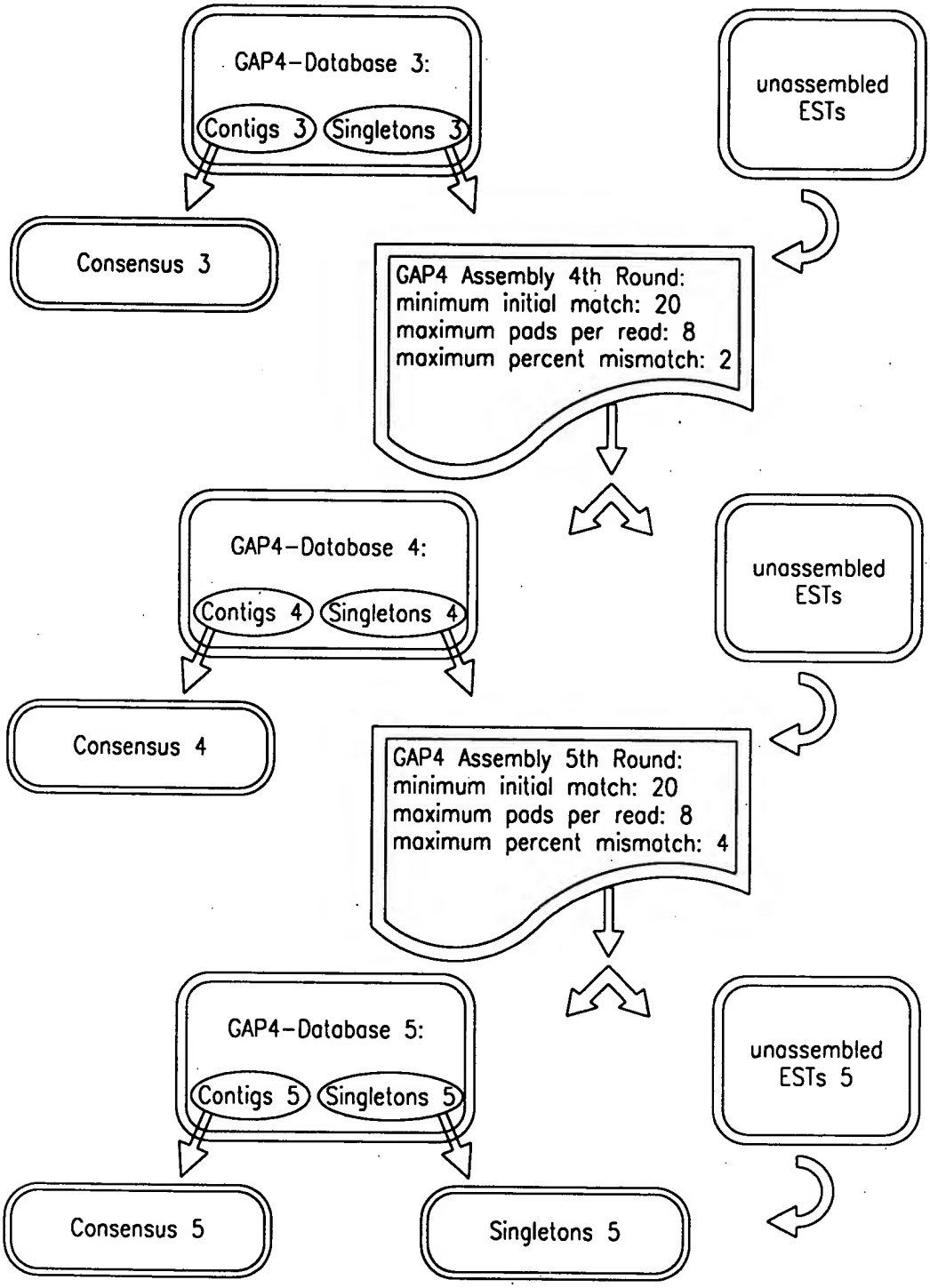


FIG. 2b-2

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

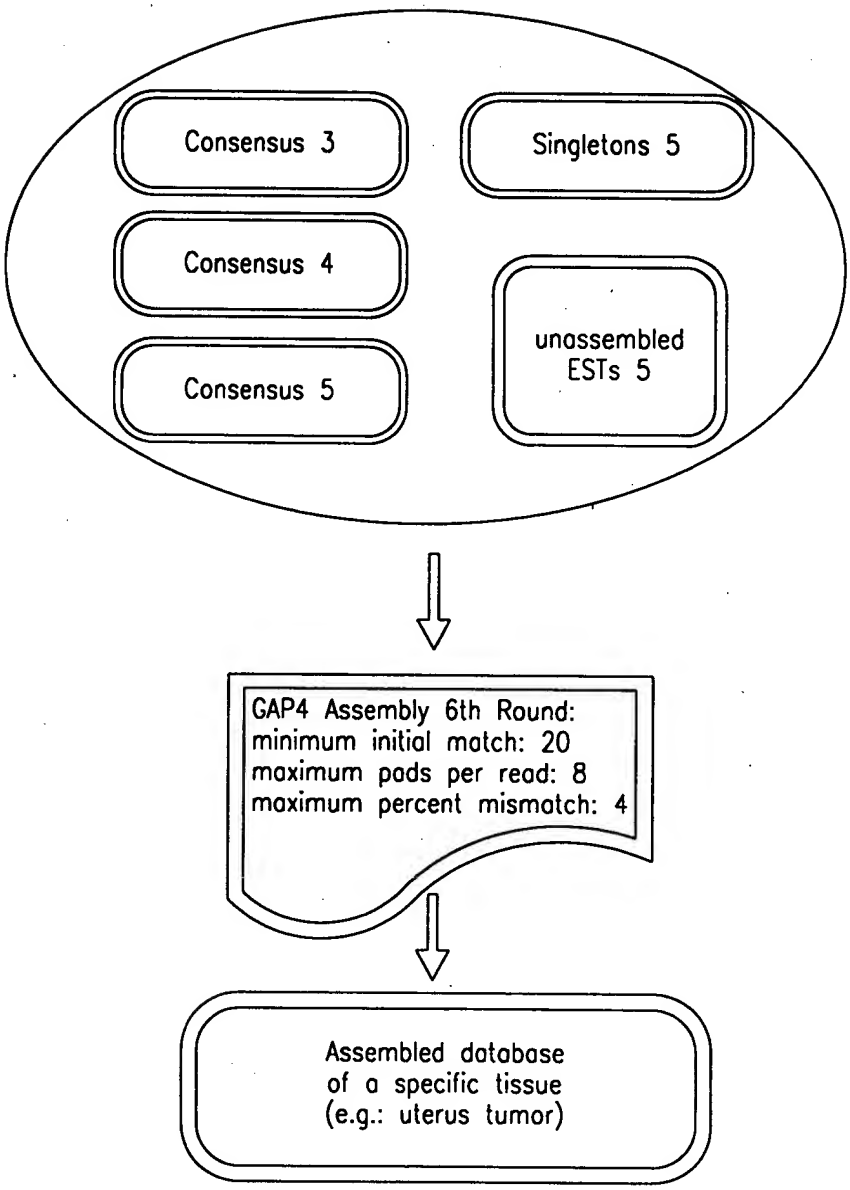


FIG. 2b-3

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

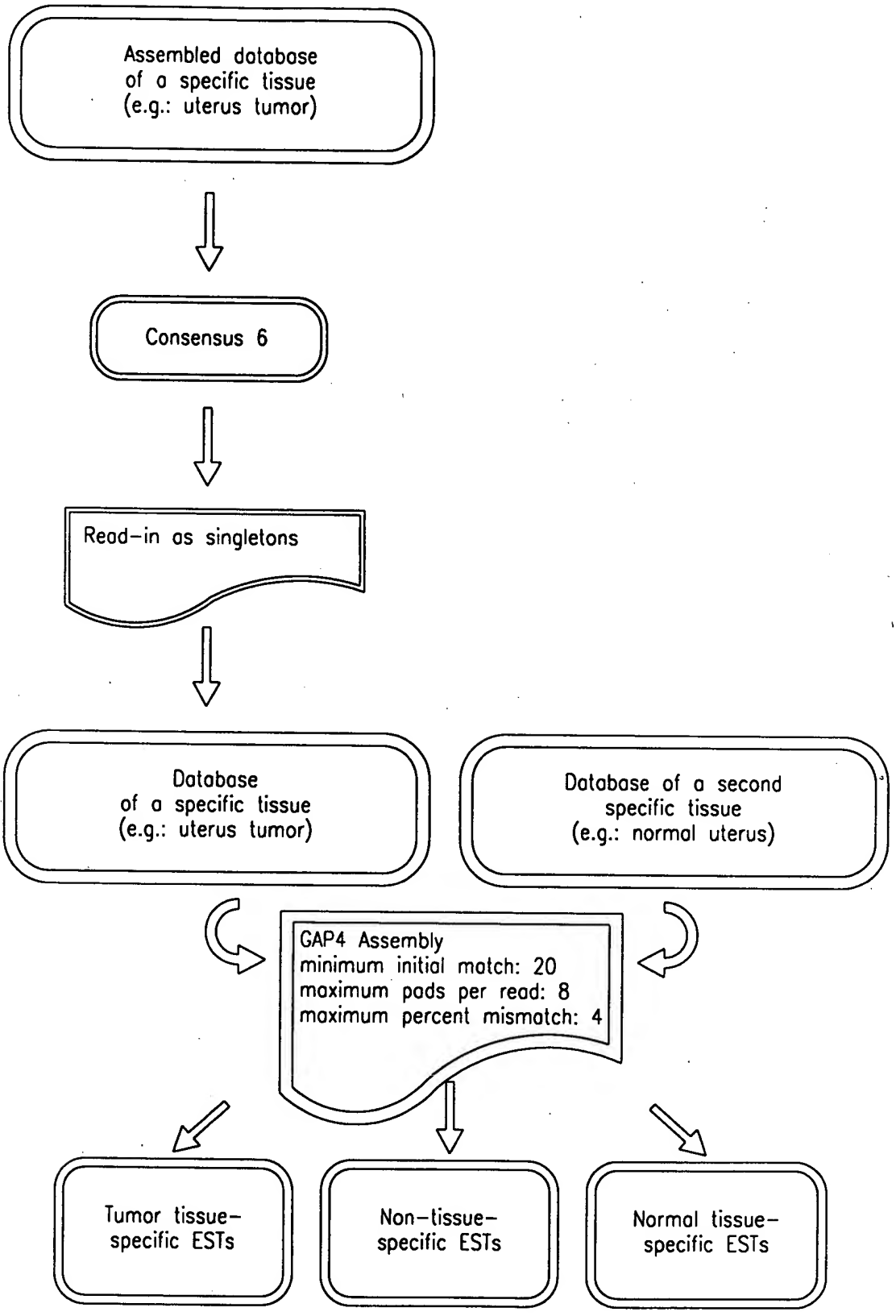


FIG. 2b-4

APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

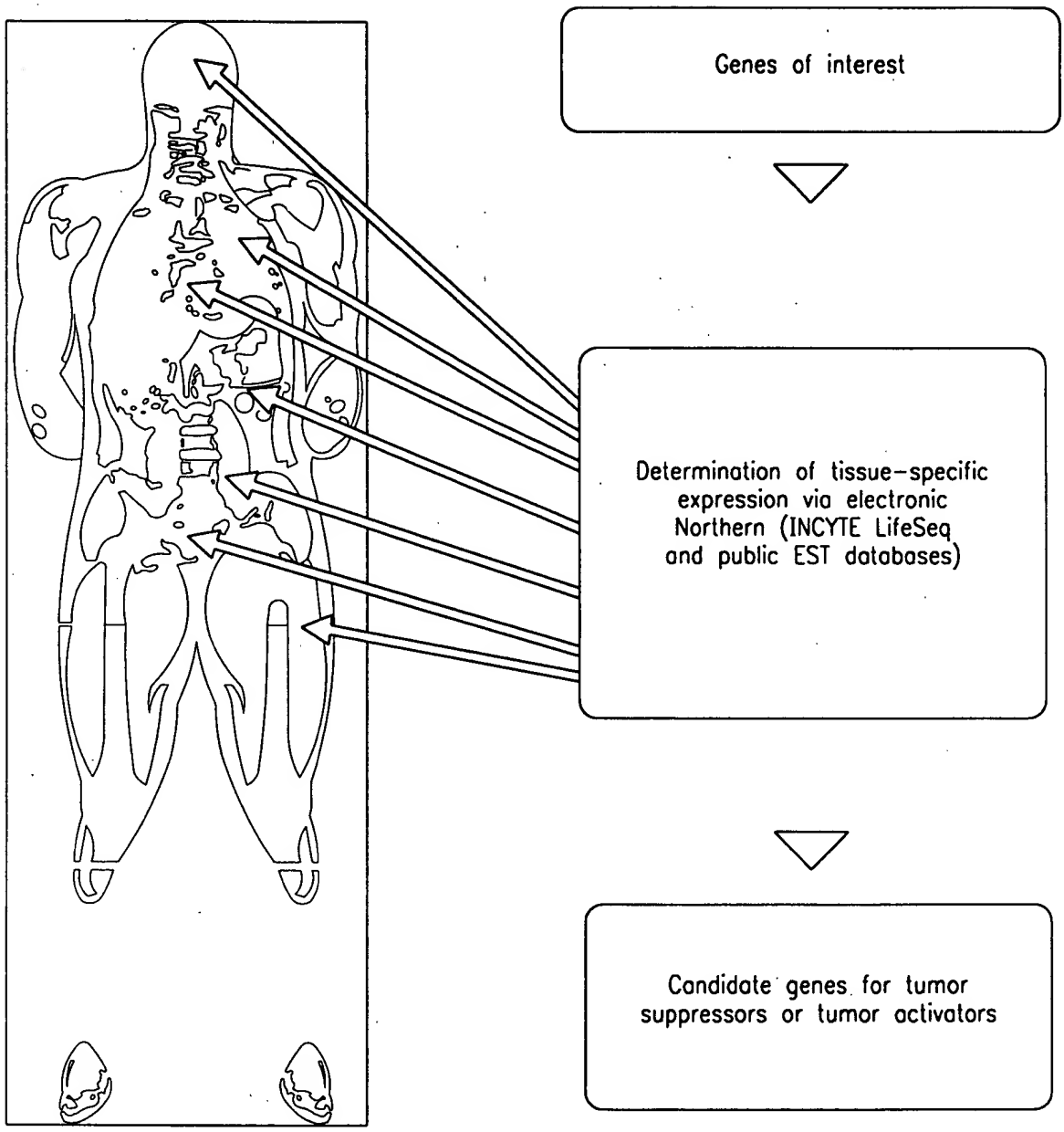


FIG. 4a

APPROVED O.G. FIG.
BY CLASS SUBCLASS
DRAFTSMAN

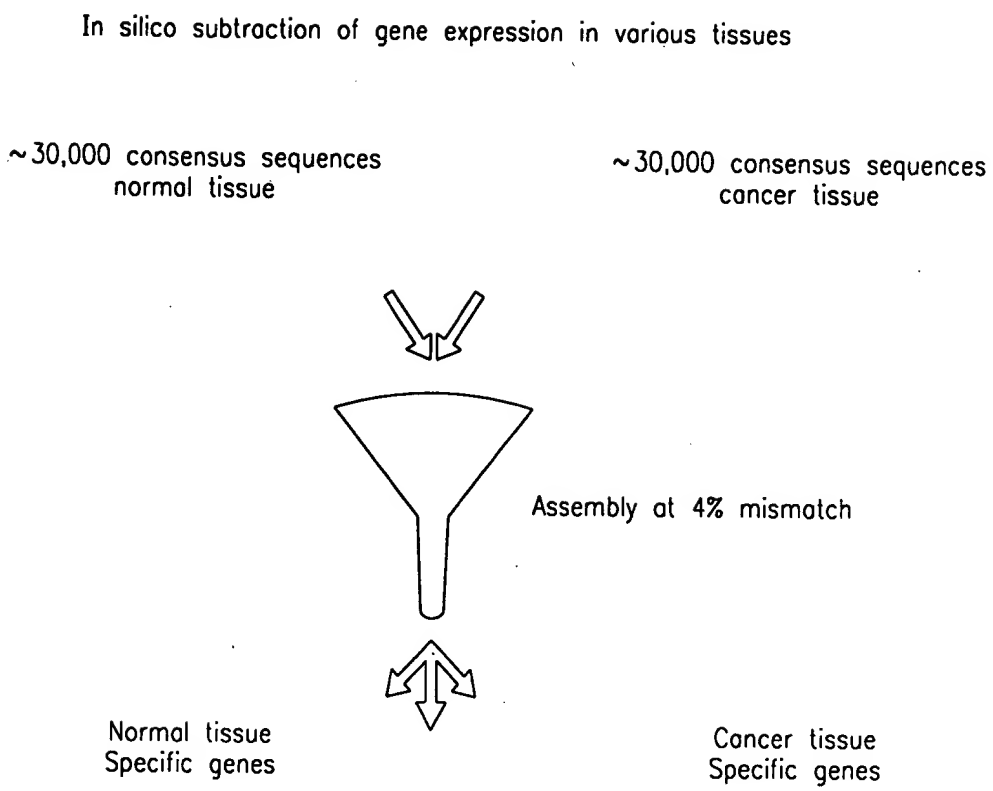


FIG. 3

APPROVED O.G. FIG.
BY CLASS SUBCLASS
DRAFTSMAN

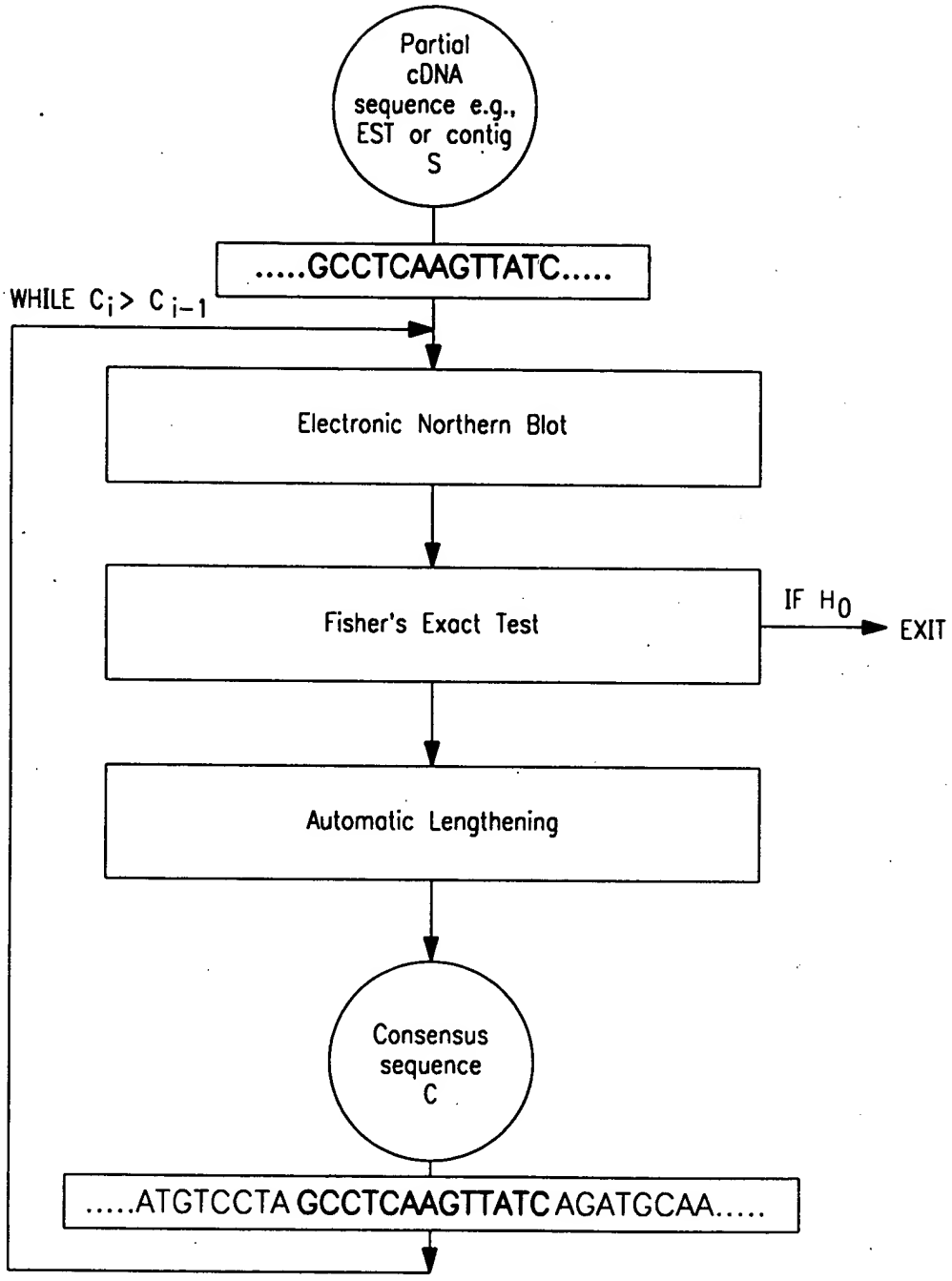


FIG. 4b

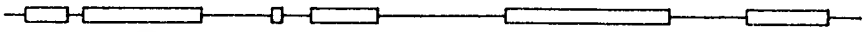
APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes



Exon Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

FIG. 5